

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file segid14vs27and28.res made by spaul on Fri 15 Aug 103 7:52:05-PDT

Query sequence being compared: US-09-581-252-14	(1-353)
Number of sequences searched:	6
Number of scores above cutoff:	6

Results of the initial comparison of US-09-581-252-14 (1-353) with
File : US09581252.pep

[illegible]

The scores below are sorted by initial score. Significance is calculated based on initial score.

2 100% identical sequences to the query sequence were found:

Sequence Name	Description	Init.	Opt.	Length	Score	Score	Sig.	Frame
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1. US-09-581-252-29 Sequence 29, Application	353	353	0.53	0
2. US-09-581-252-14 Sequence 14, Application	353	353	0.53	0

Sequence Name	Description	Length	Init. score	Opt. score	sig.	Frame
3. US-09-581-252-28	Sequence 28, Application	353	352	352	0.51	0
4. US-09-581-252-27	Sequence 27, Application	353	352	352	0.51	0
5. US-09-581-252-23	Sequence 23, Application	354	319	338	-0.03	0
	*** 1 standard deviation below mean ***					
6. US-09-581-252-15	Sequence 15, Application	213	201	202	-1.98	0

1. US-09-581-252-14 (1-353)
US-09-581-252-29 Sequence 29, Application US/09581252

Initial Score	-	353	Optimized Score	-	353	Significance	-	0.53
Residue Identity	-	100%	Matches	-	353	Mismatches	-	0
Gaps	-	0	Conservative Substitutions	-			-	0

X	10	20	30	40	50	60	70
MNECHYDKHDFEYNSNTQVDMGTGKTVILCVGTEFCLEIFFNSLVIAAIKNRFFHPPYLLANI							
MNECHYDKHDFEYNSNTQVDMGTGKTVILCVGTEFCLEIFFNSLVIAAIKNRFFHPPYLLANI							
MNECHYDKHDFEYNSNTQVDMGTGKTVILCVGTEFCLEIFFNSLVIAAIKNRFFHPPYLLANI							
X	10	20	30	40	50	60	70

80 90 100 110 120 130 140
AAAFPGIAYVFLMPTGVSXTLTITVNRWELRQGLDSSLTSLNLLYIAVERIMSSIMRRVHNSLTKKR
AAAFPGIAYVFLMPTGVSXTLTITVNRWELRQGLDSSLTSLNLLYIAVERIMSSIMRRVHNSLTKKR
80 90 100 110 120 130 140

VTLILLLMAIAIFMGAVPTLLGNCCICNISACSSLPPIYSRSLVYWTYSNLMAFLIMVYLYRLRIYVVKRRK
150 160 170 180 190 200 210

VTLILLLMAIAIFMGAVPTLLGNCCISACSSLPPIYSRSLSLVMTVSNLMAFLIMVYLRIVYVKKRRK
150 160 170 180 190 200 210

220 TTVNSPHTSGSISRRRPKMLKMTVMVLGAEVYVCMTPGILVLPEDGLNCROGQOVHVKRMFLLLALLNSVY
230 TTVNSPHTSGSISRRRPKMLKMTVMVLGAEVYVCMTPGILVLPEDGLNCROGQOVHVKRMFLLLALLNSVY
240 TTVNSPHTSGSISRRRPKMLKMTVMVLGAEVYVCMTPGILVLPEDGLNCROGQOVHVKRMFLLLALLNSVY
250 TTVNSPHTSGSISRRRPKMLKMTVMVLGAEVYVCMTPGILVLPEDGLNCROGQOVHVKRMFLLLALLNSVY
260 TTVNSPHTSGSISRRRPKMLKMTVMVLGAEVYVCMTPGILVLPEDGLNCROGQOVHVKRMFLLLALLNSVY
270 TTVNSPHTSGSISRRRPKMLKMTVMVLGAEVYVCMTPGILVLPEDGLNCROGQOVHVKRMFLLLALLNSVY
280 TTVNSPHTSGSISRRRPKMLKMTVMVLGAEVYVCMTPGILVLPEDGLNCROGQOVHVKRMFLLLALLNSVY

[illegible]

2. US-09-581-252-14 (1-353)
US-09-581-252-14 Sequence 14, Application US/09581252

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Initial Score      = 353  Optimized Score      = 353  Significance = 0.53
Residue Identity = 100%  Matches      = 353  Mismatches  = 0
Gaps              = 0    Conservative Substitutions = 0
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X 10 20 30 40 50 60 70
 MNECHYKHKHDFEYRNSRSTJVDMDTKIYLYLVCSTGFECFLIFFSNSLYAAVANKNKFHFFPYLYLANI
 MNECHYKHKHDFEYRNSRSTJVDMDTKIYLYLVCSTGFECFLIFFSNSLYAAVANKNKFHFFPYLYLANI
 X 10 20 30 40 50 60 70

AAAFPGIAVFLMFTGTGSKTLVYNNRFLNQGILDSLTSLNLLVIAVERHMSIMRRVRVSNLTKKR
80 90 100 110 120 130 140

[illegible][illegible]

Initial Score	-	352	Optimized Score	-	352	Significance	=	0.51
Residue Identity	-	99%	Matches	-	351	Mismatches	=	2
Gaps	-	0	Conservative Substitutions	-			=	0

5. US-09-581-252-14 (1-353)
US-09-581-252-23 Sequence 23, Application US/09581252

4. US-09-581-252-14 (1-353)
US-09-581-252-27 Sequence 27, Application US/09581252

Caps		-		1		Conservative Substitutions		-		8	
X	10	20	30	40	50	60	70				
MNECHYDKHMF	EYNSRNTD	VDDMTG	TKLIVL	CVGTFC	FLFIFF	SNLSLV	IAAVIK	NKRKH	HP	PYYLLANL	
MNECHYKRMDF	EYNSRNTD	PADEMTG	TKLIVL	CVGTFC	FLFIFF	SNLSLV	IAAVIT	NKRKH	FP	PYYLLANL	
X	10	20	30	40	50	60	70				
70											
70											
AAAFPGIAYFL	MFNPNG	PSKTLTY	RMFLR	GGLLDS	LTASLT	NLTYA	VERHMS	IMBRV	HSNT	TKRKR	
AAAFPGIAYFL	MFNPNG	PSKTLTY	RMFLR	GGLLDS	LTASLT	NLTYA	VERHMS	IMBRV	HSNT	TKRKR	
80	90	100	110	120	130	140					
80	90	100	110	120	130	140					
VTLLILVMAIA	FMGAVPTL	GMGLNC	ISACSS	ISAPY	RSYVFW	NTSLM	LFWVY	LVYLV	YVYV	YVYV	YVYV
150	160	170	180	190	200	210					
VTLLILVMAIA	FMGAVPTL	GMGLNC	ISACSS	ISAPY	RSYVFW	NTSLM	LFWVY	LVYLV	YVYV	YVYV	YVYV
VTLLILVMAIA	FMGAVPTL	GMGLNC	ISACSS	ISAPY	RSYVFW	NTSLM	LFWVY	LVYLV	YVYV	YVYV	YVYV
150	160	170	180	190	200	210					
VTLLILVMAIA	FMGAVPTL	GMGLNC	ISACSS	ISAPY	RSYVFW	NTSLM	LFWVY	LVYLV	YVYV	YVYV	YVYV
VTLLILVMAIA	FMGAVPTL	GMGLNC	ISACSS	ISAPY	RSYVFW	NTSLM	LFWVY	LVYLV	YVYV	YVYV	YVYV
150	160	170	180	190	200	210					
TNVLSPHTSGS	ISRRRTPM	LKMTVM	TGAFV	YVCM	TGVLV	PLDGL	NCRCQ	QVQHVK	RWFL	LALALNSV	
TNVLSPHTSGS	ISRRRTPM	LKMTVM	TGAFV	YVCM	TGVLV	PLDGL	NCRCQ	QVQHVK	RWFL	LALALNSV	
220	230	240	250	260	270	280					
TNVLSPHTSGS	ISRRRTPM	LKMTVM	TGAFV	YVCM	TGVLV	PLDGL	NCRCQ	QVQHVK	RWFL	LALALNSV	
TNVLSPHTSGS	ISRRRTPM	LKMTVM	TGAFV	YVCM	TGVLV	PLDGL	NCRCQ	QVQHVK	RWFL	LALALNSV	
220	230	240	250	260	270	280					
NPILYISKDEDM	YNTMRKMK	ICALD	OSTER	PSRPN	STIH	SRETS	QYVED	SI	QPV	CNKNKS	
NPILYISKDEDM	YNTMRKMK	ICALD	OSTER	PSRPN	STIH	SRETS	QYVED	SI	QPV	CNKNKS	
290	300	310	320	330	340	350	X				
NPILYISKDEDM	YNTMRKMK	ICALD	OSTER	PSRPN	STIH	SRETS	QYVED	SI	QPV	CNKNKS	
NPILYISKDEDM	YNTMRKMK	ICALD	OSTER	PSRPN	STIH	SRETS	QYVED	SI	QPV	CNKNKS	
290	300	310	320	330	340	350	X				
NPILYISKDEDM	YNTMRKMK	ICALD	OSTER	PSRPN	STIH	SRETS	QYVED	SI	QPV	CNKNKS	
NPILYISKDEDM	YNTMRKMK	ICALD	OSTER	PSRPN	STIH	SRETS	QYVED	SI	QPV	CNKNKS	
290	300	310	320	330	340	350	X				
NPILYISKDEDM	YNTMRKMK	ICALD	OSTER	PSRPN	STIH	SRETS	QYVED	SI	QPV	CNKNKS	

Initial Score	-	352	Optimized Score	-	352	Significance	-	0.51
Residue Identity	-	99%	Matches	-	352	Mismatches	-	0
Gaps	-	0	Conservative Substitutions	-	0		-	0
X	.10	20	30	40	50	60	70	
MNECHYDKHNDFFYNSRSTDTVDMDMTGKTLVILVCVGTFCCLFIEFSNSLVIAAVIKNRKRFHPPEYLLANT								
MNECHYDKHNDFFYNSRSTDTVDMDMTGKTLVILVCVGTFCCLFIEFSNSLVIAAVIKNRKRFHPPEYLLANT								
X	10	20	30	40	50	60	70	
MNECHYDKHNDFFYNSRSTDTVDMDMTGKTLVILVCVGTFCCLFIEFSNSLVIAAVIKNRKRFHPPEYLLANT								
X	80	90	100	110	120	130	140	
AAADFFGIAIVYFLMTGTVGSKTLVYNNRFLKQGLDSSLTASLTLLVIAVERHRSISIMRHYSLTKR								
AAADFFGIAIVYFLMTGTVGSKTLVYNNRFLKQGLDSSLTASLTLLVIAVERHRSISIMRHYSLTKR								

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5. US-09-581-252-14 (1-353)
US-09-581-252-15 Sequence 15, Application US/09581252

Initial Score = 201 Optimized Score = 202 Significance = -1.98
Residue Identity = 89% Matches = 190 Mismatches = 20
Gaps = 0 Conservative Substitutions = 3

40 50 60 70 80 90 100 110
FCCLFFFSNSLVAIVIKNRKFFPEYLLANLAADFAGIAYVFLMFYTGVSRTLTVNRRFLRQGLLD
|||||
NTGVSRTLTVNRRFLRQGLLD
X 10 20

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40      50      60      70      80      90     100     110
FECLFIFFSNSLVIAAVIKNRKFHPFPYLLANLAADFFAGIAVFLMFNTGVPYSKTLTVNRWFLROGLD
|||||
NTGVPYSKTLTVNRWFLROGLD
X      10      20

120      130      140      150      160      170      180
SSLFTSLTNLLVIAVERHMSIMRMFVHSNLTFRKRYTLILLVMAIAIFMGAVPTLGWNCICNISACSLAPI
|||||
TSLFTASLANLVIAVERHMSIMRMFVHSNLTFRKRYTLILLVMAIAIFMGAVPTLGWNCICNISACSLAPI
30      40      50      60      70      80      90

190      200      210      220      230      240      250
YRSRYLVFWTVSNLMAFLIMVYVLRIVYVYRKTNVLSPHTSGISRRRTPMKLMKTYMTVLGAFVYCWTP
|||||
YRSRYLVFWTVSNLMAFLIMVYVLRIVYVYRKTNVLSPHTSGISRRRTPMKLMKTYMTVLGAFVYCWTP
100      110      120      130      140      150      160

260      270      280      290      300      310      320
GLVYVLLDGLNCRQCGVOHVKKRMFLLLALNSVNPPIYSYKDEDMYGTMMKKMICCFSEQENPERRPSRIPST
|||||
GLVYVLLDGLNCRQCGVOHVKKRMFLLLALNSVNPPIYSYKDEDMYGTMMKKMICCFSEQENPERRPSRIPST
170      180      190      200      210 X
VLSRSDTGSQYIEDSISQGAVCNKS
330      340      350

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AAAF	80	90	100	110	120	130	140
AFGAYVYVLMNTPSPVSKTLTLMROGLDLSLTSTNLTIVAYERHMSITMRVHNSITKRR							
AAAD	80	90	100	110	120	130	140
FGIAYVFLFNMNIPSPSKITLYRKFRLROGLDLSLTSTNLTIVAYERHMSITMRVHNSITKRR							
VTLL	150	160	170	180	190	200	210
LLILVMAIIFMGAVPTLGMNCLCNISACSLAIYRSYLYVTWVSNLMAFLIMVYLRIVYVKKRR							
VTLL	150	160	170	180	190	200	210
ILVMAIIFMGAVPTLGMNCLCNISACSLAIYRSYLYVTWVSNLMAFLIMVYLRIVYVKKRR							
TNVL	220	230	240	250	260	270	280
SPHTSGSSISRRRTPKMLKTYMTVILGAFVYVCMTPGLVLLDGLNCRQGVQVHVKRWFLLALLNSVY							
TNVL	220	230	240	250	260	270	280
SPHTSGSSISRRRTPKMLKTYMTVILGAFVYVCMTPGLVLLDGLNCRQGVQVHVKRWFLLALLNSVY							
NPIT	290	300	310	320	330	340	350
YSYKDEDMGYMKKKKICFSEONERPRSPRSTPSTVSRDTSQVYEDSISOGAVCNKSTS							
NPIT	290	300	310	320	330	340	350
YSYKDEDMGYMKKKKICFSEONERPRSPRSTPSTVSRDTSQVYEDSISOGAVCNKSTS							

3. US-09-581-252-27 (1-353)
US-09-581-252-29 Sequence 29, Application US/09581252

Initial Score	-	352	Optimized Score	-	352	Significance	-	0.51
Residue Identity	-	99%	Matches	-	352	Mismatches	-	1
Gaps	-	0	Conservative Substitutions	-			-	0

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MNCCHYDKIMAEFFYKRSMTDPYDDMTGKLYIVLCVCTFEPCLEIFPNSLSLYAAVYKKNKFFHEPPYLLAAL
IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
MNECHYDKIMAEFFYKRSMTDPYDDMTGKLYIVLCVCTFEPCLEIFPNSLSLYAAVYKKNKFFHEPPYLLAAL
X      10      20      30      40      50      60      70
AAADFAGIAYVFLMNFNNGPVSKITLVYRWFELRGGCLSSLSLTAIINLVIAVERHMSIMRRVHNSNTKKR
80      90      100     110     120     130     140
AAADFAGIAYVFLMNFNNGPVSKITLVYRWFELRGGCLSSLSLTAIINLVIAVERHMSIMRRVHNSNTKKR
80      90      100     110     120     130     140

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[illegible]

4. US-09-581-252-27 (1-353)
US-09-581-252-14 Sequence 14, Application US/09581252

Initial Score	-	352	Optimized Score	-	352	Significance	-	0.51
Residue Identity	-	99%	Matches	-	352	Mismatches	-	1
Gaps	-	0	Conservative Substitutions	-	-	-	-	0

[illegible]

5. US-09-581-252-27 (1-353)
US-09-581-252-23 Sequence 23, Application US/09581252

Initial Score	=	319	Optimized Score	=	338	Significance	=	-0.03
Residue Identity	=	91%	Matches	=	323	Mismatches	=	22
Gaps	=	1	Conservative Substitutions				=	8

[illegible]

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150      160      170      180      190      200      210
VTLLILLMAIAIFMGAVTTCMNCCLINISACSSLAPIYSKSLVTFPTYSNLMALFLIMVYLIRIYVYKKRRK
VTLLILLMAIAIFMGAVTTCMNCCLINISACSSLAPIYSKSLVTFPTYSNLMALFLIMVYLIRIYVYKKRRK
150      160      170      180      190      200
VTLLILLMAIAIFMGAVTTCMNCCLINISACSSLAPIYSKSLVTFPTYSNLMALFLIMVYLIRIYVYKKRRK
220      230      240      250      260      270      280
TNVLSPIHTSGSISRRRTPKMKLTKTYMTVLGAFVYVCMTPLGLVLLLDGLNCRQCGVQHYKRWLILLALLNSVYV
TNVLSPIHTSGSISRRRTPKMKLTKTYMTVLGAFVYVCMTPLGLVLLLDGLNCRQCGVQHYKRWLILLALLNSVYV
220      230      240      250      260      270      280
TNVLSPIHTSGSISRRRTPKMKLTKTYMTVLGAFVYVCMTPLGLVLLLDGLNCRQCGVQHYKRWLILLALLNSVYV
TNVLSPIHTSGSISRRRTPKMKLTKTYMTVLGAFVYVCMTPLGLVLLLDGLNCRQCGVQHYKRWLILLALLNSVYV
290      300      310      320      330      340      350 X
NPIIYYSKDEMDYGTMKKKKICCFSEQ-NPEERSPRISITVLSRPTGSOYIEDISISQGVCKKST
NPIIYYSKDEMDYGTMKKKKICCFSEQ-NPEERSPRISITVLSRPTGSOYIEDISISQGVCKKST
NPIIYYSKDEMDYGTMKKKKICCFSEQ-NPEERSPRISITVLSRPTGSOYIEDISISQGVCKKST
290      300      310      320      330      340      350 X
NPIIYYSKDEMDYGTMKKKKICCFSEQ-NPEERSPRISITVLSRPTGSOYIEDISISQGVCKKST
NPIIYYSKDEMDYGTMKKKKICCFSEQ-NPEERSPRISITVLSRPTGSOYIEDISISQGVCKKST
NPIIYYSKDEMDYGTMKKKKICCFSEQ-NPEERSPRISITVLSRPTGSOYIEDISISQGVCKKST

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6. US-09-581-252-27 (1-353)
US-09-581-252-15 Sequence 15, Application US/09581252

Initial Score	-	202	Optimized Score	-	203	Significance	-	-1.98
Residue Identity	-	89%	Matches	-	191	Mismatches	-	19
Gaps	-	0	Conservative Substitutions				-	3

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120      130      140      150      160      170      180
SSLTASLTNLLVIAVERHMSIMRMRVHSNLTFRKRVTLTLVMAIAIFMGAVPTLGMNCLCNISACSSLAPI
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
TSLTASLTANLTVIAVERHMSIMRMRVHSNLTFRKRVTLTLVMAIAIFMGAVPTLGMNCLCNISACSSLAPI
30      40      50      60      70      80      90

190      200      210      220      230      240      250
YRSYLVFWTVSNLMAFLIMVVVYLRIVYVVKRKTNVLSPHTSGISRRRTPMKLMTVMVLGAFFVVCMTF
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
YRSYLVFWTVSNLMAFLIMVVVYLRIVYVVKRKTNVLSPHTSGISRRRTPMKLMTVMVLGAFFVVCMTF
100     110     120     130     140     150     160

260      270      280      290      300      310      320
GLVYVLPDGLNCRCQGVQHVKKRMFLILALINSVNPPIYSYKDEDMYGTMKKMICCFSGENPERRRSRIPST
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
GLVYVLLDGLNCKOCNVQHVKKRMFLILALINSVNPPIYSYKDEDMYGTMKKMICCFSGENPERRRSRIPST
170     180     190     200     210 X

330      340      350
VLSRSDTGSQYTEDSISQGAVCNKS

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